

[illegible]

1	CCTAGAGCCAGCAGAGTC	CAGGCTGCTGTTAA	CAACTTCATGTCCCCG	TGGGTAGCAGGC	60
61	AGGTGCTTCTGTCTGAT	CTGGCTCTCCTTGAC	CACTGTACTCATCAA	ATAGACCAAGATC	120
121	CCCAGAGTCCAAGATCCT	TACAAGGGGGCCAGA	AAGGGATGAGCTTTCT	GAPGAAGCACT	180
181	GATGTAAAAATACCAGGA	ATTTTGACATCGAAGA	AGATTTTGTGATGGC	AGCTGGGATTT	240
241	GGCCATAATCTAGAAGAC	ACATGGTGAATACAGT	TGCAAGTCATTTAGT	CATATTTCTTG	300
301	CTAAATTGCTGTGCTCT	CAATGGCTGAATTGA	AGATCCCTCTTACCC	GCCAGGTGCCAAG	360
361	AACTATGAACAGGCAGG	CCAATAGAAGACA	ACTAAAGAAGGATCCA	ACGATTTGAAATT	420
421	CCAGAACTTCAGTCTGC	CAAAAAACAGGTCA	TGGCCTCGCATCAAT	AGTGCCACAGGCCA	480
481	GTACCAGAGGATGAACA	AGCCTCTTCTAGACT	GGGAAAGAACTTTGT	GTCAGTCCTGGA	540
541	TGGAGCAAAAGGCCAC	AGTGATGATGACTAT	GATGACCTGAGCTTC	GGATGGAAGAGAC	600
601	ATGGCAGTCGATTAAAA	TTTTTACCAGCCCGC	CTATAAAGGAATCTG	AATATGCAGATAC	660
661	ACACTATTTCAAGGTTG	CAATGGACACTCCCCT	TCCGTTAGACACCAG	GAACCTCTATCTC	720
721	CATTGGACAGCCGACCT	TGGAACACACAGAC	GGGTTTGGAAAGAGT	TGGACAAACCCATT	780
781	CAAGGACGTCAGAAGCC	AAAAACATTAAAGG	AGATGCATCCGTAAGA	AAAGAACAGATTCC	840
841	TTTACCACCTCCTCGGC	CTCTATAACACTTCC	GAGAGTACCAACCTT	GGCCCCCTGA	900
901	GCCGGAGAGCAGCAGGC	ACCTTTATCTCAGAG	ACACCTTTCAGAA	GTCCAGAGAAAT	960
961	GCCCAGTCAGATAAGCT	TAAAGGACTTAAGT	GAGGTCCTTGAAG	CAGAAAAAGTTCT	1020
1021	TAAACAGAGGAAGCCT	GAATCAACTCATCTG	TAGAAAACAAAATA	CTCAAGAGATTCC	1080
1081	ACTTGCCATTAGCAGTT	CTTCTATTACGACA	AGCAACCACAGTGT	GCAAAACAGAGAT	1140
1141	TAGAGGAGGCATGAGC	CTGTCTCAGAGATGC	AGCCTCCAGCCAGCT	CGAGCCC	1200
1201	TCACGAAAATATACTGC	CCCTATAAAATACACA	AGCTGGAGACCACCT	TTCCCCAAAAGGTC	1260
1261	TGATAGAAAAGGATGT	CCAGCACAAATGAAT	GGTACATTGGAGAATA	CAGCCGCCAGGCAGT	1320
1321	GGAAGAGGCATTATGA	AGGAGAACAGGATGG	TAGTTTCTTGGTCCG	AGATTGTTCAC	1380
1381	AAAAATCCAAGGAAGAG	CCCTATGTTTTGGCT	GTGTTTTATGAGAAC	AAAGTCTACAATGT	1440
1441	AAAAATCCGCTTCTCG	GAGAGGAATCAGCAG	TTTGGCCTGGGGAC	AGGACTCAGAGGAGA	1500

FIG. 1B

1501 TGAGAAGTTTGATTGAGTAGAAGACATCATCGAACACTACAAGAATTTCCCATTTATACT 1560
1561 AATTGATGGGAAAAGATAAACTGGGGTCCACAGGAAACAGTGTACCTCACTCAGCCACT 1620
1621 CCCTCTACCAGACACCTCTGCCTCTGTAGCCTGGTCTTTGTGTTATCTTTGGTTTACT 1680
1681 GGATTGAGCGCTTCCATTGTTTTCATTGATTTCAAAGTTTATTTTCTGTGCCCTCAAGG 1740
1741 GACAACTTTTTTAACTTTGGAGAAAAGAAAAACACTCTATAACAGAGAGTGGAATCAC 1800
1801 TCACGGTTTGTAAAGTTCAAACACAGAGAAAATATTTATAACATGCAAAA 1851

09655-0201

FIG. 2

1		M A E L K I P L T R Q V P R	14
15	T M N R Q G N R K T T K E G S N D L K F		34
35	Q N F S L P K N R S W P R I N S A T G Q		54
55	Y Q R M N K P L L D W E R N F A A V L D		74
75	G A K G H S D D D Y D D P E L R M E E T		94
95	W Q S I K I L P A R P I K E S E Y A D T		114
115	H Y F K V A M D T P L P L D T R T S I S		134
135	I G Q P T W N T Q T R L E R V D K P I S		154
155	K D V R S Q N I K G D A S V R K N K I P		174
175	L P P P R P L I T L P K K Y Q P L P P E		194
195	P E S S R P P L S Q R H T F P E V Q R M		214
215	P S Q I S L R D L S E V L E A E K V P H		234
235	N Q R K P E S T H L L E N Q N T Q E I P		254
255	L A I S S S S F T T S N H S V Q N R D H		274
275	R G G M Q P C S P Q R C Q P P A S C S P		294
295	H E N I L P Y K Y T S W R P P F F K R S		314
315	D R K D V Q H N E W Y I G E Y S R Q A V		334
335	E E A F M K E N K D G S F L V R D C S T		354
355	K S K E E P Y V L A V F Y E N K V Y N V		374
375	K I R F L E R N Q Q F A L G T G L R G D		394
395	E K F D S V E D I I E H Y K N F P I I L		414
415	I D G K D K T G V H R K Q C H L T Q P L		434
435	P L T R H L L P L		443

FIG. 2

FIG. 3A

1	CCTAGAGCCAGCAGAGTCCAGGCTGCTGTTAACAACTTCATGTCCCCGTGGGTAGCAGGC	60
61	AGGTGCTTCTGTCTGATCTGGCTCTCCTTGACCACTGTACTCATAAATAGACCAAGATC	120
121	CCCAGAGTCCAAGATCCTTACAAGGGGGCCAGAAAGGGATGAGCTTTCTGAAGAAGCACT	180
181	GATGTAAAATACCAGGAATTTTGACATCGAAGAAGATTTTGTGATGGCAGCTGGGATTT	240
241	GGCCATAATCTAGAAGACACATGGTGAATACAGTTGCAAGTCATTTAGTCATAITTTCTTG	300
301	CTAAATGTCTGTGCTTCTCAATGGCTGAATTGAAGATCCCTCTTACCCGCCAGGTGCCAAG	360
1	M A E L K I P L T R Q V P R	14
361	AACATGAACAGGCAGGGCAATAGAAAGACAACTAAAGAAGGATCCAACGATTTGAAATT	420
15	T M N R Q G N R K T T K E G S N D L K F	34
421	CCAGAACTTCAGTCTGCCAAAAACAGGTCATGGCTCGCATCAATAGTGCCACAGGCCA	480
35	Q N F S L P K N R S W P R I N S A T G Q	54
481	GTACCAGAGGATGAACAAGCCTCTTCTAGACTGGGAAAGAACTTTGCTGCAGCTCTGGA	540
55	Y Q R M N K P L L D W E R N F A A V L D	74
541	TGGAGCAAAGGCCACAGTGATGATGACTATGATGACCTTGAGCTTCGAGTCGAAGAGAC	600
75	G A K G H S D D D Y D D P E L R M E E T	94
601	ATGGCAGTCGATTAATAATTTACCAGCCCGCCCTATAAAGGAATCTGAATATGCAGATAC	660
95	W Q S I K I L P A R P I K E S E Y A D T	114
661	ACACTATTTCAAGSTTGCAATGGGACTCCCTTCCGTTAGACACGAGACCTCTATCTC	720
115	H Y F K V A M D T P L P L D T R T S I S	134
721	CATTGGACAGCCGACCTGGAAACACAGACGAGSTTGGAAAGAGTGGACAAACCCATTTC	780
135	I G Q P T W N T Q T R L E R V D K P I S	154
781	CAAGGACGTGCAAGGCCAAAAACATTAAAGGAGATGCATCCGTAAGAAAGAACAAAGATTCC	840
155	K D V R S Q N I K G D A S V R K N K I P	174
841	TTTACCACCTCCTCGGCTCTCATAACACTTCCGAAGAAGTACCAACCTTGTCCCCCTGA	900
175	L P P P R P L I T L P K K Y Q P L P P E	194
901	GCCGGAGAGCAGCAGGCCACCTTTATCTCAGAGACACACCTTTCAGAAAGTCCAGAGAAT	960
195	P E S S R P P L S Q R H T F P E V Q R M	214
961	GCCCAAGTCAGATAAGCTTAAGGACCTAAGTGAGGTCTTTGAAGCAGAAAAAGTTCCTCA	1020
215	P S Q I S L R D L S E V L E A E K V P H	234
1021	TAACCAGAGGAAGCCTGAATCAACTCATCTGTTAGAAAAACCAAAATCTCAAGAGATTCC	1080
235	N Q R K P E S T H L L E N Q N T Q E I P	254
1081	ACTTGCCATTAGCAGTTCTTCAATTCACGACAAGCAACCAAGTGTGCAAAACAGAGATCA	1140
255	L A I S S S S F T T N H S V Q N R D H	274
1141	TAGAGGAGGCATGCAGCCCTGTTCTCTCAGAGATGCCAGCCTCCAGCCAGCTGCAGCCC	1200

0966557.02301

FIG. 3B

275	R G G M Q P C S P Q R C Q P P A S C S P	294
1201	TCACGAAAATATACTGCCCTATAAATACACAAGCTGGAGACCACCTTTCCCAAAAGGTC	1260
295	H E N I L P Y K Y T S W R P P F P K R S	314
1261	TGATAGAAAGGATGTC CAGCACAATGAATGGTACATTGGAGAATACAGCCGCCAGGCAGT	1320
315	D R K D V Q H N E W Y I G E Y S R Q A V	334
1321	GGAAGAGGCATTTCATGAAGGAGAACAGGATGGTAGTTTCTTGGTCCGAGATTGTTCCAC	1380
335	E E A F M K E N K D G S F L V R D C S T	354
1381	AAAAATCCAAGGAAGAGCCCTATGTTTTGGCTGTGTTTTATGAGAACAAAGTCTACAATGT	1440
355	K S K E E P Y V L A V F Y E N K V Y N V	374
1441	AAAAATCCGCTTCCTGGAGAGGAATCAGCAGTTTGCCTGGGGACAGGACTCAGAGGAGA	1500
375	K I R F L E R N Q Q F A L G T G L R G D	394
1501	TGAGAAGTTTGATTTCAGTAGAAGACATCATCGAACACTACAAGAATTTTCCATTATACT	1560
395	E K F D S V E D I I E H Y K N F P I I L	414
1561	AATTGATGGGAAAGATAAACTGGGGTCCACAGGAAACAGTGTACCTCACTCAGCCACT	1620
415	I D G K D K T G V H R K Q C H L T Q P L	434
1621	CCCTCTCACCAGACACCTCTTGCTCTGTAGCCTGGTCTTTGTGTTATCTTTGGTTTACT	1680
435	P L T R H L L P L *	444
1681	GGATTGAGCGCTCCATTGTTTTCATTGATTTCAAAAGTTTATTTTCTGTGCCTTCAAGG	1740
1741	GACAACTTTTTAACTTTGGAGAAAAGAAAAACACTCTATAACAGAGAGTGGAAAATCAC	1800
1801	TCACGGTTTTGAAAGTTCAAACACAGAGAAAATATTTATAACATGCAAAA	1851

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIG. 4A

1 GTGACACCTCTCAGGTCTGTGGCTGCATTTCACAGGAAACCAAGTCTAAAACGGACCTAT 60
61 CAGGAGGTTTCTGCTGAAGGGCACTGCTTAGCATCGAGAAGAATTCAACCACCGCCTT 120
121 ACTAATTTCCAGTGCCCAAGGTCTCTGCACTGCCGCCCTCTCTCACAGGAGACGGACAC 180
181 CTCAGCCTAGATCCCTTGGTGTCTCTCCACGCTGTTCAGGCTGAATTGAAGATCCCTCTTA 240
241 CCCGCCAGGTGCCAAGAAGTATGAACAGGCAGGGCAATAGAAAGACAACCTAAAGAAGGAT 300
301 CCAACGATTTGAAATTCAGAACTTCAGTCTGCCAAAAACAGGTCATGGCCTCGCATCA 360
361 ATAGTGCCACAGGCCAGTACCAGAGGATGAACAAGCCTCTTCTAGACTGGGAAAGAACT 420
421 TTGCTGCAGTCTGTGGATGGAGCAAAAGGCCACAGTGATGATGACTATGATGACCTTGAGC 480
481 TTCGGATGGAAGAGACATGGCAGTCGATTAAAATTTACACGCCCGGCTTATAAGGAAT 540
541 CTGAATATGCAGATACACACTATTTCAAGTTGCAATGGACACTCCCCTTCGGTTAGACA 600
601 CCAGGACCTCTATCTCCATTGGACAGCCGACCTGGAACACACAGACGAGGTTGGAAGAG 660
661 TGGACAAACCCATTTCCAAGGACGTGAGAAGCCAAACATTAAAGGAGATGCATCCGTAA 720
721 GAAAGAACAAGATTCTTTACCACCTCCTCGGCCTCTCATAACACTTCCGAAGAAGTACC 780
781 AACCCTTGCCCTTGAGCCGGAGAGCAGCAGGCCACCTTTATCTCAGAGACACACCTTTC 840
841 CAGAAGTCCAGAGAATGCCAGTCAGATAAGCTTAAGGGACTTAAGTGAGTCTTTGAAG 900
901 CAGAAAAAGTTCTCATAACCAGAGGAAGCCTGAATCAACTCATCTGTTAGAAAAACAAA 960
961 ATACTCAAGAGATTCACCTTGCCATTAGCAGTTCCTCATTCACGACAAGCAACCACAGTG 1020
1021 TGCAAAACAGAGATCATAGAGGAGGCATGCAGCCCTGTTCTCCTCAGAGATGCCAGCCTC 1080
1081 CAGCCAGCTGCAGCCCTCACGAAATATACTGCCCATAAATACACAAGCTGGAGACCAC 1140
1141 CTTTCCCCAAAAGGTCTGATAGAAAAGGATGTCCAGCACAAATGAATGGTACATTGGAGAAT 1200
1201 ACAGCCGCCAGGCAGTGGAAGAGGCATTTCATGAAGGAGAACAAGGATGGTAGTTTCTTGG 1260
1261 TCCGAGATTGTTCCACAAAATCCAAGGAAGAGCCCTATGTTTTGGCTGTGTTTTATGAGA 1320
1321 ACAAAGTCTACAATGTAAAAATCCGCTTCTCGAGAGGAAATCAGCAGTTTGCCCTGGGGA 1380
1381 CAGGACTCAGAGGAGATGAGAAGTTTGATTTCAGTAGAAGACATCATCGAACACTACAAGA 1440

096695.092004

FIG. 5

09956955-092801

1		M N R Q G N R K T T K E G S	14
15	N D L K F Q N F S L P K N R S W P R I N		34
35	S A T G Q Y Q R M N K P L L D W E R N F		54
55	A A V L D G A K G H S D D D Y D D P E L		74
75	R M E E T W Q S I K I L P A R P I K E S		94
95	E Y A D T H Y F K V A M D T P L P L D T		114
115	R T S I S I G Q P T W N T Q T R L E R V		134
135	D K P I S K D V R S Q N I K G D A S V R		154
155	K N K I P L P P P R P L I T L P K K Y Q		174
175	P L P P E P E S S R P P L S Q R H T F P		194
195	E V Q R M P S Q I S L R D L S E V L E A		214
215	E K V P H N Q R K P E S T H L L E N Q N		234
235	T Q E I P L A I S S S S F T T S N H S V		254
255	Q N R D H R G G M Q P C S P Q R C Q P P		274
275	A S C S P H E N I L P Y K Y T S W R P P		294
295	F P K R S D R K D V Q H N E W Y I G E Y		314
315	S R Q A V E E A F M K E N K D G S F L V		334
335	R D C S T K S K E E P Y V L A V F Y E N		354
355	K V Y N V K I R F L E R N Q Q F A L G T		374
375	G L R G D E K F D S V E D I I E H Y K N		394
395	F P I I L I D G K D K T G V H R K Q C H		414
415	L T Q P L P L T R H L L P L		428

FIG. 6A

1	GTCAGACCTCTCAGGTCTGTGGCTGCATTTACAGGAAACCAAGTCTAAAACGGACCTAT	60
61	CAGGAGGTTTCTGCTGAAGGGCACTGCTTAGCATCGAGAAGAATTCAACCCACCGCCTT	120
121	ACTAATTTCCAGTGCCCAAGGTCTCTGCACTGCCGCCCTCCTCACAGGAGACGGACAC	180
181	CTCAGCCTAGATCCCTTGGTGTCTCCACGTGTTCAGGCTGAATTGAAGATCCCTCTTA	240
241	CCCGCCAGGTGCCAAGAACTATGAACAGGCAGGGAATAGAAAGACAACATAAAGAGGAT	300
1	M N R Q G N R K T T K E G S	14
301	CCAACGATTTGAAATTCAGAACTTCAGTCTGCCAAAAACAGGTCTAGGCCCTCGCATCA	360
15	N D L K F Q N F S L P K N R S W P R I N	34
361	ATAGTGCCACAGGCCAGTACCAGAGGATGAACAAGCCTCTTCTAGACTGGAAAGAACT	420
35	S A T G Q Y Q R M N K P L L D W E R N F	54
421	TTGCTGCAGTCTGGATGGAGCAAAAGGCCACAGTGATGATGACTATGATGACCTGAGC	480
55	A A V L D G A K G H S D D D Y D D P E L	74
481	TTCCGATGGAAGAGACATGGCAGTCGATTAATTTTACCAGCCCGCCTATAAAGGAAT	540
75	R M E E T W Q S I K I L P A R P I K E S	94
541	CTGAATATGCAGATACACACTATTTCAAGGTTGCAATGGACACTCCCTTCCGTTAGACA	600
95	E Y A D T H Y F K V A M D T P L P L D T	114
601	CCAGGACCTCTATCTCCATTGGACAGCCGACCTGGAACACACAGACGAGGTTGGAAGAG	660
115	R T S I S I G Q P T W N T Q T R L E R V	134
661	TGGACAAACCCATTTCCAAGGACGTCAGAAGCCAAAACATTAAGGAGATGCATCCGTAA	720
135	D K P I S K D V R S Q N I K G D A S V R	154
721	GAAAGAACAAGATTCTTTTACCACCTCTCGGCCTCTCATAACACTTCCGAAGAAGTACC	780
155	K N K I P L P P P R P L I T L P K K Y Q	174
781	AACCTTTGCCCTTGGCCGGAGAGCAGCAGGCCACCTTTATCTCAGAGACACACCTTTC	840
175	P L P P E P E S S R P P L S Q R H T F P	194
841	CAGAAGTCCAGAGAATGCCAGTCAGATAAGCTTAAGGGACTTAAGTGAGGTCCTTGAAG	900
195	E V Q R M P S Q I S L R D L S E V L E A	214
901	CAGAAAAAGTTCTCTATAACAGAGGAAGCCTGAATCAACTCATCTGTGTAGAAAACCAA	960
215	E K V P H N Q R K P E S T H L L E N Q N	234
961	ATACTCAAGAGATTCCACTTGCCATTAGCAGTTCTTCATTACGACACAGCAACCACAGTG	1020
235	T Q E I P L A I S S S S F T T S N H S V	254
1021	TGCAAAACAGAGATCATAGAGGAGGCATGCAGCCCTGTTCTCCTCAGAGATGCCAGCCTC	1080
255	Q N R D H R G G M Q P C S P Q R C Q P P	274
1081	CAGCCAGCTGCAGCCCTCACGAAAATATACTGCCCTATAAATACACAAGCTGGAGACCAC	1140
275	A S C S P H E N I L P Y K Y T S W R P P	294

006655-03201

FIG. 6B

1141	CTTTCCCCAAAAGGTCTGATAGAAAAGGATGTCAGCACAAATGAATGGTACATTGGAGAAT	1200
295	F P K R S D R K D V Q H N E W Y I G E Y	314
1201	ACAGCCGCCAGGCAGTGAAGAGGCATTCATGAAGGAGAACAAGGATGGTAGTTCTTGG	1260
315	S R Q A V E E A F M K E N K D G S F L V	334
1261	TCCGAGATTGTTCCACAAAATCCAAGGAAGAGCCCTATGTTTGGCTGTGTTTATGAGA	1320
335	R D C S T K S K E E P Y V L A V F Y E N	354
1321	ACAAAGTCTACAATGTAAAAATCCGCTTCCTGGAGAGGAATCAGCAGTTTGCCTGGGGA	1380
355	K V Y N V K I R F L E R N Q Q F A L G T	374
1381	CAGGACTCAGAGGAGATGAGAAGTTTGATTTCAGTAGAAGACATCATCGAACACTACAAGA	1440
375	G L R G D E K F D S V E D I I E H Y K N	394
1441	ATTTTCCCATTATACTAATTGATGGGAAAGATAAAAATGGGGTCCACAGGAACAGTGTG	1500
395	F P I I L I D G K D K T G V H R K Q C H	414
1501	ACCTCACTCAGCCACTCCCTCTCACCAGACACCTCTTGCTGTAGCCTGGTCTTTGTG	1560
415	L T Q P L P L T R H L L P L	429
1561	TTATCTTTGGTTTACTGGATTTCAGCGCTTCCATTGTTTTCATTGATTTCAAAGTTTAT	1620
1621	TTCTGTGCCTTCAAGGGACAACTTTTTTAACCTTTGGAGAAAAGAAAACACTCTATAACA	1680
1681	GAGAGTGGAAAATCACTCACGGTTTGAAGTTCAAACACAGAGAAAATATTTATAACA	1740
1741	TGCAAAAAATAAAAAACATTCTAGTAACCTGGCCACTGGAAAATAAATAAAAAATAAACTA	1800
1801	GGGTTTTAAAGTATCTTCTAAAAAACAAACAAAAATACTATAAACATAGCCATTAT	1860
1861	GCTCATGATACAGGCGAGCAGCAAAGGGCACCAGAAGCTGTGCTTAAATGTTTGCACTC	1920
1921	AGTGCAAGACAAGTCTATGGGAAATTCCTCAATCTGTGCTCTTTACAGGACACTGCGCTG	1980
1981	CCTTTATGTGAGTTGTTGGGCCTTACATATATACAATGTGTGGATGATTCTTACACTAA	2040
2041	AGATGCTGGGCTGGGTGCGGTGCTCATGCTGTAATCCCGACACTTTGGGAGGCTGAGG	2100
2101	TGGACAGATACGAGGTCAGGAGATCAAGACCATCCTGGCTAACATGGTGAAACCCCATG	2160
2161	TCTACTAAAAATACAAAAATCAGCTGGGCGTGGTGGTGGGTGCCTGTAGTCCCAGCTAC	2220
2221	TCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCGAGCTTGCACTGAGCCGA	2280
2281	AATCGCGCCACTGCCTCCAATCCAGCCTGGGACAGAGAGACTCCGCTCTCAAA	2335

CGCGGCTGGGCTGGGTGCGGTGCTCATGCTGTAATCCCGACACTTTGGGAGGCTGAGG

FIG. 7A

1 GGCTGCTGTTAAACAACCTCATGTCCCCGTGGGTAGCAGGCAGGTGCTTCTGTCTGATCTG 60
61 GCTCTCCTTGACCACTGTACTCATCAAATAGACCAAGATCCCCAGAGTCCAAGATCCTTA 120
121 CAAGGGGGCCAGAAAGGGATGAGCTTTCTGAAGAAGCACTGATGTAAAATACCAGGAATT 180
181 TTGACATCGAAGAAGATTTTTGTGTATGGCAGCTGGGATTTGCCATAATCTAGAAGACAC 240
241 ATGGTGAATACAGTTGCAAGTCATTTAGTCATATTTCTTGCTAAATTGCTGTGCTTCAA 300
301 TGGGGCAATAGAAAGACAACATAAGAAGGATCCAACGATTTGAAATTCAGAACCTCAGT 360
361 CTGCCAAAAACAGGTCATGGCCTCGCATCAATAGTGCCACAGGCCAGTACCAGAGGATG 420
421 AACAGCCTCTTCTAGACTGGATTGGCAGCTTGACCATTTATTATCGCACAGTGGATGC 480
481 AATCAGAAGTCTGGGCACAGCATGGCTCAACTAGTTCCTCTGCTGGGTCTCACAAGAC 540
541 TGAAAGCAACATGCTGGCAGGGCTGCATTCTCTCCAGGGGCTCTGAAGAGGAACCTTGCT 600
601 TCCAGATTCTTTCAGGAAAGAACTTTGCTGCAGTCTCGATGGAGCAAAAGGCCACAGT 660
661 GATGATGACTATGATGACCTTGAGCTTCGGATGGAAGAGACATGGCAGTCGATTAAAATT 720
721 TTACCAGCCCGCCTATAAAGGAATCTGAATATGCAGATACACACTATTTCAAGGTTGCA 780
781 ATGGACACTCCCCCTCCGTTAGACACCAGGACCTCTATCTCCATTGGACAGCCGACCTGG 840
841 AACACACAGACGAGGTTGGAAGAGTGGACAAACCCATTTCGAAGACGTCAGAAGCCAA 900
901 AACATTAAAGGAGATGCATCCGTAAGAAAGAAACAAGATTCCCTTTACCACCTCCTCGGCCT 960
961 CTCATAACACTTCCGAAGAAGTACCAACCCCTTGCCCCCTGAGCCGGAGAGCAGCAGGCCA 1020
1021 CCTTTATCTCAGAGACACACCTTTCCAGAAGTCCAGAGAATGCCAGTCAGATAAGCTTA 1080
1081 AGGGACTTAAGTGAGGTCTTGAAGCAGAAAAAGTTCCATCATAACCAGAGGAAGCCTGAA 1140
1141 TCAACTCATCTGTTAGAAAACCAAATACTCAAGAGATTCCACTTGCCATTAGCAGTTCT 1200
1201 TCATTACGACAAGCAACCACAGTGTGCAAAACAGAGATCATAGAGGAGGCATGCAGCCC 1260
1261 TGTTCCTCTCAGAGATGCCAGCCTCCAGCCAGCTGCAGCCCTCACGAAAAATATACTGCC 1320
1321 TATAAATACACAAGCTGGAGACCACCTTTCCCCAAAAGGTCTGATAGAAAGGATGTCCAG 1380
1381 CACAATGAANTGGTACATTGGAGAATACAGCCGCCAGGCAGTGAAGAGGCATTCATGAAG 1440

095655.07201

FIG. 8

1 M E E T W Q S I K I 10
 11 L P A R P I K E S E Y A D T H Y F K V A 30
 31 M D T P L P L D T R T S I S I G Q P T W 50
 51 N T Q T R L E R V D K P I S K D V R S Q 70
 71 N I K G D A S V R K N K I P L P P P R P 90
 91 L I T L P K K Y Q P L P P E P E S S R P 110
 111 P L S Q R H T F P E V Q R M P S Q I S L 130
 131 R D L S E V L E A E K V P H N Q R K P E 150
 151 S T H L L E N Q N T Q E I P L A I S S S 170
 171 S F T T S N H S V Q N R D H R G G M Q P 190
 191 C S P Q R C Q P P A S C S P H E N I L P 210
 211 Y K Y T S W R P P F P K R S D R K D V Q 230
 231 H N E W Y I G E Y S R Q A V E E A F M K 250
 251 E N K D G S F L V R D C S T K S K E E P 270
 271 Y V L A V F Y E N K V Y N V K I R F L E 290
 291 R N Q Q F A L G T G L R G D E K F D S V 310
 311 E D I I E H Y K N F P I I L I D G K D K 330
 331 T G V H R K Q C H L T Q P L P L T R H L 350
 351 L P L 353

00965955.002801

FIG. 9A

1	GGCTGCTGTAAACAACITTCATGTCCCCTGGGTAGCAGGCAGGTGCTTCTGTCTGATCTG	60
61	GCTCTCCTTGACCACGTGTACTCATCAATAGACCAAGATCCCAGAGTCCAAGATCCTTA	120
121	CAAGGGGGCCAGAAAGGGATGAGCTTTCTGAAGAAGCACTGATGTAATAACACAGGAATT	180
181	TTGACATCGAAGAAGATTTTTGATGGCAGCTGGGATTGGCCATAATCTAGAAGACAC	240
241	ATGTTGAATACAGTTGCAAGTCATTTAGTCATATTTCTGCTAAATGCTGTCTCTTCAA	300
301	TGGGGCAATAGAAAGACAACCTAAAGAAGGATCCAACGATTTGAAATTCAGAACTTCAGT	360
361	CTGCCAAAAACAGGTTCATGGCCTCGCATCAATAGTGCCACAGGCCAGTACCAGAGGATG	420
421	AACAAGCCTCTTCTAGACTGGATTGGCAGCTTGACCATTATTTATCGCACAGTGGATGC	480
481	AATCAGAAGTCTGGGCACAGCATGGCTCAACTAGTTCCCCCTGTTCTGGGTCTCACAAAGAC	540
541	TGAAAGCAACATGCTGGCAGGGCTGCATTCTCTCCAGGGCTCTGAAGAGGAAGTCTGCT	600
601	TCCGATTCTTTTCAGGAAAGAACTTTGCTGTCAGTCTGGATGGAGCAAAGGCCACAGT	660
661	GATGATGACTATGATGACCTGAGCTTCGGATGGAAGAGACATGGCAGTCGATTAATAAT	720
1	M E E T W Q S I K I	10
721	TTACCAGCCCGGCCTATAAAGGAATCTGAATATGCAGATACACACTATTTCAAGTTGCA	780
11	L P A R P I K E S E Y A D T H Y F K V A	30
781	ATGGACACTCCCTTCCGTTAGACACCAGGACCTCTATCTCCATTGGACAGCCGACCTGG	840
31	M D T T P L P L D T R T S I S I G Q P T W	50
841	AACACACAGACGAGTTGGAAGAGTGGACAAACCCATTTCCAAGGACGTGAGAAGCCAA	900
51	N T Q T R L E R V D K P I S K D V R S Q	70
901	AACATTAAAGGAGATGCATCCGTGAAGAAAGAAAGAGATTCTTTACACCTCTCTGGCCCT	960
71	N I K G D A S V R K N K I P L P P P R P	90
961	CTCATAACACTTCCGAAGAAGTACCAACCTTGCCCCCTGAGCCGGAGAGCAGCAGGCCA	1020
91	L I T L P K K Y Q P L P P E P E S S R P	110
1021	CCTTTATCTCAGAGACACACCTTCCAGAGTCCAGAGAATGCCAGTCAAGTAAAGCTTA	1080
111	P L S Q R H T F P E V Q R M P S Q I S L	130
1081	AGGGACTTAAGTGAGGTCTTGAAGCAGAAAAAGTTCTCATAACCAAGGAAGCCTGAA	1140
131	R D L S E V L E A E K V P H N Q R K P E	150
1141	TCAACTCATCTGTTAGAAAAACCAAAATCTCAAGAGATTCCTACTGCCATTAGCAGTTCT	1200
151	S T H L L E N Q N T Q E I P L A I S S S	170
1201	TCATTACAGCAAGCAACCACAGTGTGCAAAACAGAGATCATAGAGAGGCATGACGCC	1260
171	S F T T S N H S V Q N R D H R G G M Q P	190
1261	TGTTCTCCTCAGAGATGCCAGCCTCCAGCCAGCTGCAGCCCTCACGAAAATACTGCCC	1320

CC66955.072301

FIG. 9B

191	C S P Q R C Q P P A S C S P H E N I L P	210
1321	TATAAATACACAGCTGGAGACCACCTTCCCCAAAGGTCTGATAGAAAGGATGTCCAG	1380
211	Y K Y T S W R P P F P K R S D R K D V Q	230
1381	CACAATGAATGGTACATTGGAGAATACAGCCGCCAGGCAGTGGGAAGAGGCATTTCATGAAG	1440
231	H N E W Y I G E Y S R Q A V E E A F M K	250
1441	GAGAACAAGGATGGTAGTTTCTTGGTCCGAGATTGTTCCACAAAATCCAAGGAAGAGCCCC	1500
251	E N K D G S F L V R D C S T K S K E E P	270
1501	TATGTTTTGGCTGTGTTTTATGAGAACAAAGTCTACAATGTAAAAATCCGCTTCTCTGGAG	1560
271	Y V L A V F Y E N K V Y N V K I R F L E	290
1561	AGGAATCAGCAGTTTGGCCCTGGGGCAGGACTCAGAGGAGATGAGAAGTTTGATTCAGTA	1620
291	R N Q Q F A L G T G L R G D E K F D S V	310
1621	GAAGACATCATCGAACACTACAAGAATTTTCCATTATACTAATTGATGGGAAAGATAAA	1680
311	E D I I E H Y K N F P I I L I D G K D K	330
1681	ACTGGGGTCCACAGGAAACAGTGTCACTCACTCAGCCATCCCTCTCACCAGACACCTC	1740
331	T G V H R K Q C H L T Q P L P L T R H L	350
1741	TTGCCCTCTGAGCCCTGGTCTTTGTGTTATCTTTGGTTTACTGGATTACAGCGCTCCATTG	1800
351	L P L *	354
1801	TTTTATTGATTTCAAAAGTTTATTTTCTGTGCCTTCAAGGGACAACCTTTTTTAACTTTG	1860
1861	GAGAAAAGAAAAACACTCTATAACAGAGAGTGGAAAATCACTCAGCGTTTTTGAAAGTTCA	1920
1921	AACCACAGAGAAAAATTTTATAACATGCAAAAAATAAAAAATTCTAGTAACGGCCACT	1980
1981	GGAAAAATAATAAAAAATAAACTAGGGTTTTAAAGTATCTTCTAAAAACAACAACAA	2040
2041	AAAACTACTATAAACATAGCCATTATGCTCATGATACAGCGAGCAGCAAAAGGACACCAGA	2100
2101	AGCTGTTGCTTAAATGTTTGCACTCAGTGCAAGACAAGTCTATGGGAAATTTCCCAATCT	2160
2161	GTGCTCTTTACAGGACACTGCGCTGCCTTTATGTCAGTTGTTGGGCCTTACATATATACA	2220
2221	ATGTGTGGATGATTTCTTACACTAAAGATGCTGGGCTGGGTGCGGTGCCTCATGCCTGTA	2280
2281	ATCCCAGCACTTTGGGAGGCTGAGGTGGACAGATCACGAGGTCAGGAGATCAAGACCATC	2340
2341	CTGGCTAACATGTTGAAACCCCATGTCTACTAAAAATACAAAAATCAGCTGGGCGTGGT	2400
2401	GGTGGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCG	2460
2461	GGAGGCGAGCTTGCAGTGAGCGGAAATCGCGCCACTGCACTCCAATCCAGCTGGGGAC	2520
2521	AGAGAGACTCCGTCTCAAAA	2540

0056055.09201

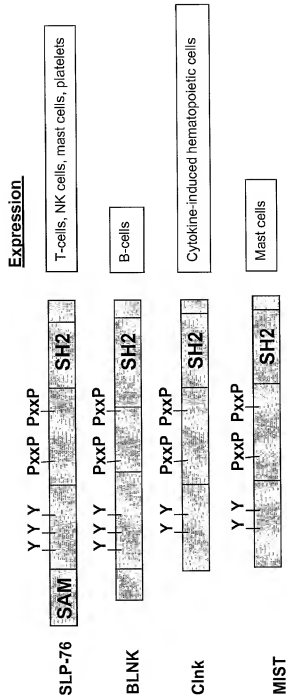


FIG. 10

FIG. 11
Recombinant MIST proteins

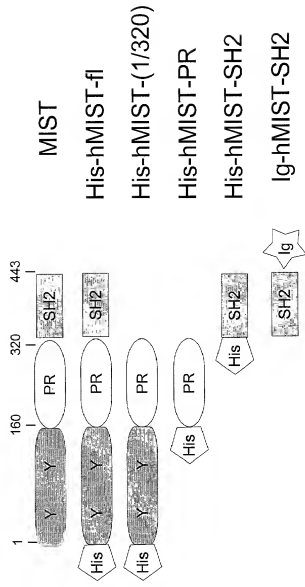
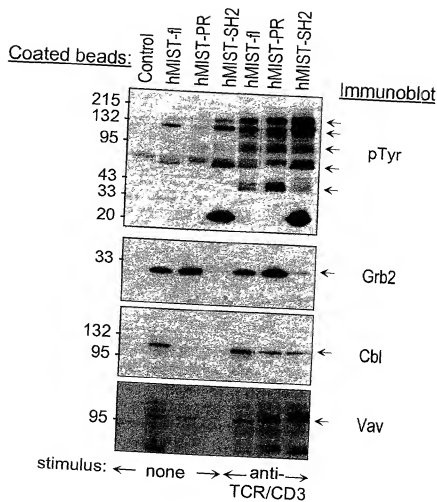


FIG. 12



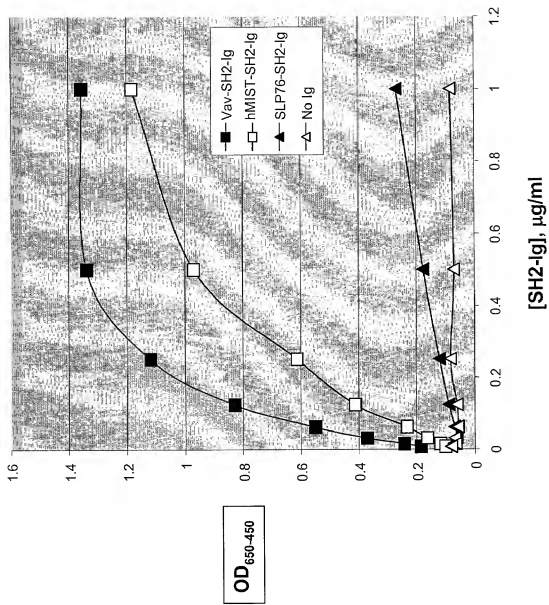


FIG. 14



FIG. 15A

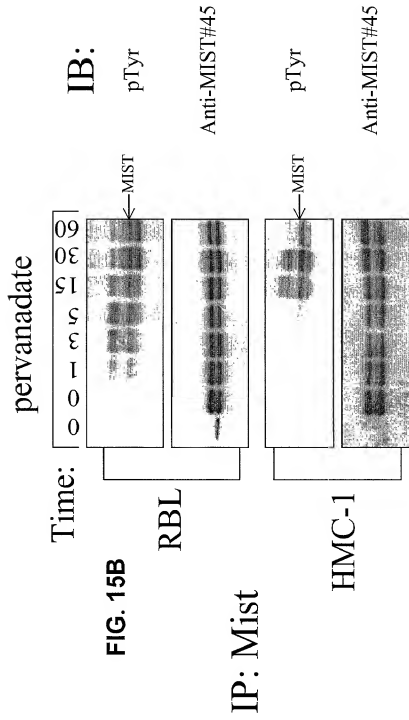


FIG. 15B